



Sequence Listing

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Presta, Leonard G.
Shelton, David L.
Urfer, Roman

(ii) TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor Inhibitors

(iii) NUMBER OF SEQUENCES: 41

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear
(B) STREET: 620 Newport Center Drive 16th Floor
(C) CITY: Newport Beach
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92660

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: 09/724,524
(B) FILING DATE: 27-NOV-2000
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/156,923
(B) FILING DATE: 18-SEP-1998
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/359,705
(B) FILING DATE: 20-DEC-1994
(C) CLASSIFICATION:

(ix) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/286846
(B) FILING DATE: 10-AUG-1994

(x) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/215139
(B) FILING DATE: 18-MAR-1994

(xi) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dreger, Ginger
(B) REGISTRATION NUMBER: 33,055
(C) REFERENCE/DOCKET NUMBER: GENENT.33CP2C2

(x) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 949/760-0404
- (B) TELEFAX: 949/760-9502

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3194 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAAGGTTTA AAGAAGAAC CGCAAAAGCGC AGGGAAAGGCC TCCCGGCACG 50
GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100
CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150
CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200
TTCGCCGTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250
CGACCCCTTCT CCTGGCATCG TGGCATTTC GAGATTGGAG CCTAACAGTG 300
TAGATCCTGA GAACATCACCA GAAATTTCA TCGCAAACCA GAAAAGGTTA 350
GAAATCATCA ACGAAGATGA TGTTGAAGCT TATGTGGGAC TGAGAAATCT 400
GACAATTGTG GATTCTGGAT TAAAATTGT GGCTCATAAA GCATTCTGA 450
AAAACAGCAA CCTGCAGCAC ATCAATTAA CCCGAAACAA ACTGACGAGT 500
TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550
GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600
AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650
AGCAGCAAGA ATATTCCCCT GGCAAACCTG CAGATAACCA ATTGTGGTT 700
GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750
CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800
TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850
ACAGGGCTCC TTAAGGATAA CTAACATTTC ATCCGATGAC AGTGGGAAGC 900
AGATCTCTTG TGTGGCGGAA AATCTGTAG GAGAAGATCA AGATTCTGTC 950
AACCTCACTG TGCATTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000
CTCAGACCAC CACTGGTGCA TTCCATTACAC TGTGAAAGGC AACCCAAAAC 1050

CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100
ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150
CCAGCTGGAT AATCCCACTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200
CCAAGAACATGA GTATGGGAAG GATGAGAAC AGATTCTGC TCACTTCATG 1250
GGCTGGCCTG GAATTGACGA TGTTGCAAAC CCAAATTATC CTGATGTAAT 1300
TTATGAAGAT TATGGAAC TG CAGCGAATGA CATCGGGAC ACCACGAACA 1350
GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTGGGAA 1400
CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTG 1450
CCTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTG 1500
GCATGAAAGG CCCAGCCTCC GTTATCAGCA ATGATGATGA CTCTGCCAGC 1550
CCACTCCATC ACATCTCCAA TGGGAGTAAC ACTCCATCTT CTTCGGAAGG 1600
TGGCCCAGAT GCTGTCATTA TTGGAATGAC CAAGATCCCT GTCATTGAAA 1650
ATCCCCAGTA CTTTGGCATH ACCAACAGTC AGCTCAAGCC AGACACATT 1700
GTTCAGCACA TCAAGCGACA TAACATTGTT CTGAAAAGGG AGCTAGGGCA 1750
AGGAGCCTT GGAAAAGTGT TCCTAGCTGA ATGCTATAAC CTCTGTCCTG 1800
AGCAGGACAA GATCTTGGTG GCAGTGAAGA CCCTGAAGGA TGCCAGTGAC 1850
AATGCACGCA AGGACTTCCA CCGTGAGGCC GAGCTCCTGA CCAACCTCCA 1900
GCATGAGCAC ATCGTCAAGT TCTATGGCGT CTGCGTGGAG GGCGACCCCC 1950
TCATCATGGT CTTTGAGTAC ATGAAGCATG GGGACCTCAA CAAGTTCCCTC 2000
AGGGCACACG GCCCTGATGC CGTGCTGATG GCTGAGGGCA ACCCGCCAC 2050
GGAAC TGACG CAGTCGCAGA TGCTGCATAT AGCCCAGCAG ATCGCCGCGG 2100
GCATGGTCTA CCTGGCGTCC CAGCACTTCG TGCACCGCGA TTTGGCCACC 2150

AGGAAC TGCGGGGA GAACTTGCTG GTGAAAATCG GGGACTTTGG 2200
GATGTCCCGG GACGTGTACA GCACTGACTA CTACAGGGTC GGTGGCCACA 2250
CAATGCTGCC CATTGCTGG ATGCCTCCAG AGAGCATCAT GTACAGGAAA 2300
TTCACGACGG AAAGCGACGT CTGGAGCCTG GGGGTCGTGT TGTGGGAGAT 2350
TTTCACCTAT GGCAAAACAGC CCTGGTACCA GCTGTCAAAC AATGAGGTGA 2400
TAGAGTGTAT CACTCAGGGC CGAGTCCTGC AGCGACCCCCG CACGTGCC 2450
CAGGAGGTGT ATGAGCTGAT GCTGGGGTGC TGGCAGCGAG AGCCCCACAT 2500

GAGGAAGAAC ATCAAGGGCA TCCATACCCCT CCTTCAGAAC TTGGCCAAGG 2550
CATCTCCGGT CTACCTGGAC ATTCTAGGCT AGGGCCCTTT TCCCCAGACC 2600
GATCCTTCCC AACGTACTCC TCAGACGGGC TGAGAGGATG AACATCTTT 2650
AACTGCCGCT GGAGGCCACC AAGCTGCTCT CCTTCACTCT GACAGTATTAA 2700
ACATCAAAGA CTCCGAGAAG CTCTCGAGGG AAGCAGTGTG TACTTCTTCA 2750
TCCATAGACA CAGTATTGAC TTCTTTTG CATTATCTCT TTCTCTCTT 2800
CCATCTCCCT TGGTTGTTCC TTTTCTTT TTTAAATTAA CTTTTCTTC 2850
TTTTTTTCG TCTTCCCTGC TTCACGATTTC TTACCCCTTC TTTTGAATCA 2900
ATCTGGCTTC TGCATTACTA TTAACCTCTGC ATAGACAAAG GCCTTAACAA 2950
ACGTAATTG TTATATCAGC AGACACTCCA GTTGTCCCAC CACAACTAAC 3000
AATGCCTTGT TGTATTCTG CCTTTGATGT GGATGAAAAA AAGGGAAAAC 3050
AAATATTCA CTTAAACTTT GTCACCTCTG CTGTACAGAT ATCGAGAGTT 3100
TCTATGGATT CACTTCTATT TATTTATTAT TATTACTGTT CTTATTGTTT 3150
TTGGATGGCT TAAGCCTGTG TATAAAAAAA AAAAAAAATC TAGA 3194

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 822 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu
1				5				10					15	
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe
				20			25						30	
Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys
				35				40					45	
Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro
				50				55					60	
Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn
				65				70					75	
Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr
				80			85						90	
Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe

95	100	105
Val Ala His Lys Ala Phe Leu Lys Asn Ser Asn Leu Gln His Ile 110	115	120
Asn Phe Thr Arg Asn Lys Leu Thr Ser Leu Ser Arg Lys His Phe 125	130	135
Arg His Leu Asp Leu Ser Glu Leu Ile Leu Val Gly Asn Pro Phe 140	145	150
Thr Cys Ser Cys Asp Ile Met Trp Ile Lys Thr Leu Gln Glu Ala 155	160	165
Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys Leu Asn Glu Ser 170	175	180
Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro Asn Cys Gly 185	190	195
Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val Glu Glu 200	205	210
Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp Pro Val 215	220	225
Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met 230	235	240
Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile 245	250	255
Ser Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn 260	265	270
Leu Val Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe 275	280	285
Ala Pro Thr Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His 290	295	300
Trp Cys Ile Pro Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu 305	310	315
Gln Trp Phe Tyr Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile 320	325	330
Cys Thr Lys Ile His Val Thr Asn His Thr Glu Tyr His Gly Cys 335	340	345
Leu Gln Leu Asp Asn Pro Thr His Met Asn Asn Gly Asp Tyr Thr 350	355	360
Leu Ile Ala Lys Asn Glu Tyr Gly Lys Asp Glu Lys Gln Ile Ser 365	370	375
Ala His Phe Met Gly Trp Pro Gly Ile Asp Asp Gly Ala Asn Pro		

380	385	390
Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr Gly Thr Ala Ala Asn 395	400	405
Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu Ile Pro Ser Thr 410	415	420
Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser Val Tyr Ala 425	430	435
Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val Met 440	445	450
Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys 455	460	465
Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro 470	475	480
Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu 485	490	495
Gly Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val 500	505	510
Ile Glu Asn Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys 515	520	525
Pro Asp Thr Phe Val Gln His Ile Lys Arg His Asn Ile Val Leu 530	535	540
Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala 545	550	555
Glu Cys Tyr Asn Leu Cys Pro Glu Gln Asp Lys Ile Leu Val Ala 560	565	570
Val Lys Thr Leu Lys Asp Ala Ser Asp Asn Ala Arg Lys Asp Phe 575	580	585
His Arg Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu His Ile 590	595	600
Val Lys Phe Tyr Gly Val Cys Val Glu Gly Asp Pro Leu Ile Met 605	610	615
Val Phe Glu Tyr Met Lys His Gly Asp Leu Asn Lys Phe Leu Arg 620	625	630
Ala His Gly Pro Asp Ala Val Leu Met Ala Glu Gly Asn Pro Pro 635	640	645
Thr Glu Leu Thr Gln Ser Gln Met Leu His Ile Ala Gln Gln Ile 650	655	660
Ala Ala Gly Met Val Tyr Leu Ala Ser Gln His Phe Val His Arg		

665	670	675
Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Leu Leu Val		
680	685	690
Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr Ser Thr Asp		
695	700	705
Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg Trp Met		
710	715	720
Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp		
725	730	735
Val Trp Ser Leu Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly		
740	745	750
Lys Gln Pro Trp Tyr Gln Leu Ser Asn Asn Glu Val Ile Glu Cys		
755	760	765
Ile Thr Gln Gly Arg Val Leu Gln Arg Pro Arg Thr Cys Pro Gln		
770	775	780
Glu Val Tyr Glu Leu Met Leu Gly Cys Trp Gln Arg Glu Pro His		
785	790	795
Met Arg Lys Asn Ile Lys Gly Ile His Thr Leu Leu Gln Asn Leu		
800	805	810
Ala Lys Ala Ser Pro Val Tyr Leu Asp Ile Leu Gly		
815	820	822

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1870 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAAGGTTTA AAGAAGAACG CGCAAAGCGC AGGGAAAGGCC TCCCAGCACG 50

GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100

CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150

CGCGGCTCTG GGGCTCTGC TGGCTGGTG TGGCTTCTG GAGGGCCGCT 200

TTCCGCCTGTC CCACGTCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250

CGACCCTTCT CCTGGCATCG TGGCATTCC GAGATTGGAG CCTAACAGTG 300

TAGATCCTGA GAACATCACC GAAATTTCA TCGCAAACCA GAAAAGGTTA 350

GAAATCATCA ACGAAGATGA TGGTGAAGCT TATGTGGGAC TGAGAAATCT 400
GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450
AAAACAGCAA CCTGCAGCAC ATCAATTAA CCCGAAACAA ACTGACGAGT 500
TTGTCTAGGA AACATTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550
GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600
AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650
AGCAGCAAGA ATATTCCCCT GGCAAAACCTG CAGATAACCA ATTGTGGTT 700
GCCATCTGCA AATCTGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750
CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800
TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850
ACAGGGCTCC TTAAGGATAA CTAACATTTC ATCCGATGAC AGTGGGAAGC 900
AGATCTCTTG TGTGGCGGAA AATCTTGTAG GAGAAGATCA AGATTCTGTC 950
AACCTCACTG TGCATTTGC ACCAACTATC ACATTCTCG AATCTCCAAC 1000
CTCAGACCAC CACTGGTGCA TTCCATTACAC TGTGAAAGGC AACCCAAAAC 1050
CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100
ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150
CCAGCTGGAT AATCCCACTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200
CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTCTGC TCACCTCATG 1250
GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300
TTATGAAGAT TATGGAACGT CAGCGAATGA CATCGGGGAC ACCACGAACA 1350
GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400
CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTG 1450

CCTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTG 1500
GCATGAAAGG TTTGTTTG TTTCTAAAGA TCCCACGGG TGGTAGCTG 1550
AAATAAAGGA AAAGACAGAG AAAGGGGCTG TGGTGCTTGT TGGTTGATGC 1600
TGCCATGTAA GCTGGACTCC TGGGACTGCT GTTGGCTTAT CCCGGGAAGT 1650
GCTGCTTATC TGGGGTTTC TGGTAGATGT GGGCGGTGTT TGGAGGCTGT 1700
ACTATATGAA GCCTGCATAT ACTGTGAGCT GTGATTGGGG AACACCAATG 1750
CAGAGGTAAC TCTCAGGCAG CTAAGCAGCA CCTCAAGAAA ACATGTTAAA 1800

TTAATGCTTC TCTTCTTACA GTAGTTCAAA TACAAAATG AAATGAAATC 1850

CCATTGGATT GTACTTCTCT 1870

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Ser Trp Ile Arg Trp His Gly Pro Ala Met Ala Arg Leu
1 5 10 15

Trp Gly Phe Cys Trp Leu Val Val Gly Phe Trp Arg Ala Ala Phe
20 25 30

Ala Cys Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys
35 40 45

Ser Asp Pro Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro
50 55 60

Asn Ser Val Asp Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn
65 70 75

Gln Lys Arg Leu Glu Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr
80 85 90

Val Gly Leu Arg Asn Leu Thr Ile Val Asp Ser Gly Leu Lys Phe
95 100 105

Val Ala His Lys Ala Phe Leu Lys Asn Ser Asn Leu Gln His Ile
110 115 120

Asn Phe Thr Arg Asn Lys Leu Thr Ser Leu Ser Arg Lys His Phe
125 130 135

Arg His Leu Asp Leu Ser Glu Leu Ile Leu Val Gly Asn Pro Phe
140 145 150

Thr Cys Ser Cys Asp Ile Met Trp Ile Lys Thr Leu Gln Glu Ala
155 160 165

Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys Leu Asn Glu Ser
170 175 180

Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro Asn Cys Gly
185 190 195

Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val Glu Glu
200 205 210

Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp Pro Val

215	220	225
Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met		
230	235	240
Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile		
245	250	255
Ser Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn		
260	265	270
Leu Val Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe		
275	280	285
Ala Pro Thr Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His		
290	295	300
Trp Cys Ile Pro Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu		
305	310	315
Gln Trp Phe Tyr Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile		
320	325	330
Cys Thr Lys Ile His Val Thr Asn His Thr Glu Tyr His Gly Cys		
335	340	345
Leu Gln Leu Asp Asn Pro Thr His Met Asn Asn Gly Asp Tyr Thr		
350	355	360
Leu Ile Ala Lys Asn Glu Tyr Gly Lys Asp Glu Lys Gln Ile Ser		
365	370	375
Ala His Phe Met Gly Trp Pro Gly Ile Asp Asp Gly Ala Asn Pro		
380	385	390
Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr Gly Thr Ala Ala Asn		
395	400	405
Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu Ile Pro Ser Thr		
410	415	420
Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser Val Tyr Ala		
425	430	435
Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val Met		
440	445	450
Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys		
455	460	465
Gly Phe Val Leu Phe His Lys Ile Pro Leu Asp Gly		
470	475	477

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2715 base pairs

- (B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTGTAGTTT 50
CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100
TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150
CGGCGGCCGG ACGATGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTG 200
AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250
ATATCACTTC CATAACACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300
GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350
CTCAGGACTT CGGAGCATTC AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400
TGCCTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450
CTCTTCCAGA CGCTGAGTCT TCGGGATTG CAGTTGGAGC AGAACTTTT 500
CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550
AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600
CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650
CAGCGTGAGC CACGTCAACC TGACCGTAGG AGAGGGTGAC AATGCTGTTA 700
TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750
ACTGGGCTGC AGTCCATCAA CACTCACCAAG ACCAATCTGA ACTGGACCAA 800
TGTTCATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850
GCTTCACCCCT GACGTGCATT GCAGAGAACG TGGTGGCAT GAGCAATGCC 900

AGTGTGCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950
GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTGTGGTG CGTGGCAACC 1000
CCCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050
AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATT CCGAGGGCTG 1100
CCTGCTCTTC AACAAAGCCA CCCACTACAA CAATGGCAAC TATACCCCTCA 1150
TTGCCAAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200
CTCAAGGAGC CCTTTCCAGA GAGCACGGAT AACTTATCT TGTTGACGA 1250

AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300
CTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTGC CTGTGTCCCTG 1350
TTGGTGGTTC TCTTCGTCA GATCAACAAA TATGGTCGAC GGTCAAATT 1400
TGGAAATGAAG GGTCCCGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450
GCCCACTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCACTGGAT 1500
GCCGGGCCCG ACACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550
GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600
ATGTGCAGCA CATTAAGAGG AGAGACATCG TGCTGAAGCG AGAACTGGGT 1650
GAGGGAGCCT TTGGAAAGGT CTTCCGGCC GAGTGCTACA ACCTCAGCCC 1700
GACCAAGGAC AAGATGCTTG TGGCTGTGAA GGCCCTGAAG GATCCCACCC 1750
TGGCTGCCCG GAAGGATTTC CAGAGGGAGG CCGAGCTGCT CACCAACCTG 1800
CAGCATGAGC ACATTGTCAA GTTCTATGGA GTGTGCGGCG ATGGGGACCC 1850
CCTCATCATG GTCTTGAAT ACATGAAGCA TGGAGACCTG AATAAGTTCC 1900
TCAGGGCCCA TGGGCCAGAT GCAATGATCC TTGTGGATGG ACAGCCACGC 1950
CAGGCCAAGG GTGAGCTGGG GCTCTCCAA ATGCTCCACA TTGCCAGTCA 2000
GATGCCCTCG GGTATGGTGT ACCTGGCCTC CCAGCACTTT GTGCACCGAG 2050
ACCTGGCAC CAGGAACCTGC CTGGTTGGAG CGAATCTGCT AGTGAAGATT 2100
GGGGACTTCG GCATGTCCAG AGATGTCTAC AGCACGGATT ATTACAGGCT 2150
CTTTAATCCA TCTGGAAATG ATTTTGAT ATGGTGTGAG GTGGGAGGAC 2200
ACACCATGCT CCCCATTCGC TGGATGCCCTC CTGAAAGCAT CATGTACCGG 2250
AAGTCACTA CAGAGAGTGA TGTATGGAGC TTCGGGGTGA TCCTCTGGGA 2300
GATCTCACC TATGGAAAGC AGCCATGGTT CCAACTCTCA AACACGGAGG 2350

TCATTGAGTG CATTACCCAA GGTCGTGTTT TGGAGCGGCC CCGAGTCTGC 2400
CCCAAAGAGG TGTACGATGT CATGCTGGGG TGCTGGCAGA GGGAACACACA 2450
GCAGCGGTTG AACATCAAGG AGATCTACAA AATCCTCCAT GCTTGGGGA 2500
AGGCCACCCC AATCTACCTG GACATTCTTG GCTAGTGGTG GCTGGTGGTC 2550
ATGAATTCAT ACTCTGTGCTCCTCCTC CCTGCCCTCAC ATCTCCCTTC 2600
CACCTCACAA CTCCCTCCAT CCTTGACTGA AGCGAACATC TTCATATAAA 2650
CTCAAGTGCC TGCTACACAT ACAACACTGA AAAAAGGAAA AAAAAAGAAA 2700

AAAAAAAAAA ACCGC 2715

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile
1				5				10					15	
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu
				20				25					30	
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys
				35				40				45		
Arg	Arg	Pro	Asp	Asp	Gly	Asn	Leu	Phe	Pro	Leu	Leu	Glu	Gly	Gln
				50				55				60		
Asp	Ser	Gly	Asn	Ser	Asn	Gly	Asn	Ala	Asn	Ile	Asn	Ile	Thr	Asp
				65				70				75		
Ile	Ser	Arg	Asn	Ile	Thr	Ser	Ile	His	Ile	Glu	Asn	Trp	Arg	Ser
				80				85				90		
Leu	His	Thr	Leu	Asn	Ala	Val	Asp	Met	Glu	Leu	Tyr	Thr	Gly	Leu
				95				100				105		
Gln	Lys	Leu	Thr	Ile	Lys	Asn	Ser	Gly	Leu	Arg	Ser	Ile	Gln	Pro
				110				115				120		
Arg	Ala	Phe	Ala	Lys	Asn	Pro	His	Leu	Arg	Tyr	Ile	Asn	Leu	Ser
				125				130				135		
Ser	Asn	Arg	Leu	Thr	Thr	Leu	Ser	Trp	Gln	Leu	Phe	Gln	Thr	Leu
				140				145				150		
Ser	Leu	Arg	Glu	Leu	Gln	Leu	Glu	Gln	Asn	Phe	Phe	Asn	Cys	Ser
				155				160				165		
Cys	Asp	Ile	Arg	Trp	Met	Gln	Leu	Trp	Gln	Glu	Gln	Gly	Glu	Ala
				170				175				180		
Lys	Leu	Asn	Ser	Gln	Asn	Leu	Tyr	Cys	Ile	Asn	Ala	Asp	Gly	Ser
				185				190				195		
Gln	Leu	Pro	Leu	Phe	Arg	Met	Asn	Ile	Ser	Gln	Cys	Asp	Leu	Pro
				200				205				210		
Glu	Ile	Ser	Val	Ser	His	Val	Asn	Leu	Thr	Val	Arg	Glu	Gly	Asp
				215				220				225		

Asn Ala Val Ile Thr Cys Asn Gly Ser Gly Ser Pro Leu Pro Asp		
230	235	240
Val Asp Trp Ile Val Thr Gly Leu Gln Ser Ile Asn Thr His Gln		
245	250	255
Thr Asn Leu Asn Trp Thr Asn Val His Ala Ile Asn Leu Thr Leu		
260	265	270
Val Asn Val Thr Ser Glu Asp Asn Gly Phe Thr Leu Thr Cys Ile		
275	280	285
Ala Glu Asn Val Val Gly Met Ser Asn Ala Ser Val Ala Leu Thr		
290	295	300
Val Tyr Tyr Pro Pro Arg Val Val Ser Leu Glu Glu Pro Glu Leu		
305	310	315
Arg Leu Glu His Cys Ile Glu Phe Val Val Arg Gly Asn Pro Pro		
320	325	330
Pro Thr Leu His Trp Leu His Asn Gly Gln Pro Leu Arg Glu Ser		
335	340	345
Lys Ile Ile His Val Glu Tyr Tyr Gln Glu Gly Glu Ile Ser Glu		
350	355	360
Gly Cys Leu Leu Phe Asn Lys Pro Thr His Tyr Asn Asn Gly Asn		
365	370	375
Tyr Thr Leu Ile Ala Lys Asn Pro Leu Gly Thr Ala Asn Gln Thr		
380	385	390
Ile Asn Gly His Phe Leu Lys Glu Pro Phe Pro Glu Ser Thr Asp		
395	400	405
Asn Phe Ile Leu Phe Asp Glu Val Ser Pro Thr Pro Pro Ile Thr		
410	415	420
Val Thr His Lys Pro Glu Glu Asp Thr Phe Gly Val Ser Ile Ala		
425	430	435
Val Gly Leu Ala Ala Phe Ala Cys Val Leu Leu Val Val Leu Phe		
440	445	450
Val Met Ile Asn Lys Tyr Gly Arg Arg Ser Lys Phe Gly Met Lys		
455	460	465
Gly Pro Val Ala Val Ile Ser Gly Glu Glu Asp Ser Ala Ser Pro		
470	475	480
Leu His His Ile Asn His Gly Ile Thr Thr Pro Ser Ser Leu Asp		
485	490	495
Ala Gly Pro Asp Thr Val Val Ile Gly Met Thr Arg Ile Pro Val		
500	505	510

Ile	Glu	Asn	Pro	Gln	Tyr	Phe	Arg	Gln	Gly	His	Asn	Cys	His	Lys
515														525
Pro	Asp	Thr	Tyr	Val	Gln	His	Ile	Lys	Arg	Arg	Asp	Ile	Val	Leu
530														540
Lys	Arg	Glu	Leu	Gly	Glu	Gly	Ala	Phe	Gly	Lys	Val	Phe	Leu	Ala
545														555
Glu	Cys	Tyr	Asn	Leu	Ser	Pro	Thr	Lys	Asp	Lys	Met	Leu	Val	Ala
560														570
Val	Lys	Ala	Leu	Lys	Asp	Pro	Thr	Leu	Ala	Ala	Arg	Lys	Asp	Phe
575														585
Gln	Arg	Glu	Ala	Glu	Leu	Leu	Thr	Asn	Leu	Gln	His	Glu	His	Ile
590														600
Val	Lys	Phe	Tyr	Gly	Val	Cys	Gly	Asp	Gly	Asp	Pro	Leu	Ile	Met
605														615
Val	Phe	Glu	Tyr	Met	Lys	His	Gly	Asp	Leu	Asn	Lys	Phe	Leu	Arg
620														630
Ala	His	Gly	Pro	Asp	Ala	Met	Ile	Leu	Val	Asp	Gly	Gln	Pro	Arg
635														645
Gln	Ala	Lys	Gly	Glu	Leu	Gly	Leu	Ser	Gln	Met	Leu	His	Ile	Ala
650														660
Ser	Gln	Ile	Ala	Ser	Gly	Met	Val	Tyr	Leu	Ala	Ser	Gln	His	Phe
665														675
Val	His	Arg	Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Ala	Asn
680														690
Leu	Leu	Val	Lys	Ile	Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Val	Tyr
695														705
Ser	Thr	Asp	Tyr	Tyr	Arg	Leu	Phe	Asn	Pro	Ser	Gly	Asn	Asp	Phe
710														720
<u>Cys</u>	<u>Ile</u>	<u>Trp</u>	<u>Cys</u>	<u>Glu</u>	<u>Val</u>	<u>Gly</u>	<u>Gly</u>	<u>His</u>	<u>Thr</u>	<u>Met</u>	<u>Leu</u>	<u>Pro</u>	<u>Ile</u>	<u>Arg</u>
725														735
Trp	Met	Pro	Pro	Glu	Ser	Ile	Met	Tyr	Arg	Lys	Phe	Thr	Thr	Glu
740														750
Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Ile	Leu	Trp	Glu	Ile	Phe	Thr
755														765
Tyr	Gly	Lys	Gln	Pro	Trp	Phe	Gln	Leu	Ser	Asn	Thr	Glu	Val	Ile
770														780
Glu	Cys	Ile	Thr	Gln	Gly	Arg	Val	Leu	Glu	Arg	Pro	Arg	Val	Cys
785														795

Pro Lys Glu Val Tyr Asp Val Met Leu Gly Cys Trp Gln Arg Glu
800 805 810

Pro Gln Gln Arg Leu Asn Ile Lys Glu Ile Tyr Lys Ile Leu His
815 820 825

Ala Leu Gly Lys Ala Thr Pro Ile Tyr Leu Asp Ile Leu Gly
830 835 839

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1858 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTGTAGTTT 50
CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100
TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150
CGGCGGCCGG ACGATGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200
AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250
ATATCACTTC CATAACACATA GAGAACTGGC GCAGTCTTCA CACGCTAAC 300
GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350
CTCAGGACTT CGGAGCATTC AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400
TGCCTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450
CTCTTCCAGA CGCTGAGTCT TCGGGATTG CAGTTGGAGC AGAACTTTT 500
CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550
AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600
CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650
CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700
TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750
ACTGGGCTGC AGTCCATCAA CACTCACCAAG ACCAATCTGA ACTGGACCAA 800
TGTTCATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850
GCTTCACCCCT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900
AGTGTGCCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950

GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTGTGGTG CGTGGCAACC 1000
CCCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050
AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100
CCTGCTCTTC AACAAAGCCCA CCCACTACAA CAATGGCAAC TATACCCCTCA 1150
TTGCCAAAAA CCCACTGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200
CTCAAGGAGC CCTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250
AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300
CTTTTGGGT ATCCATAGCA GTTGGACTTG CTGCTTTGC CTGTGTCCCTG 1350
TTGGTGGTTC TCTTCGTCA GATCAACAAA TATGGTCGAC GGTCAAATT 1400
TGGAATGAAG GGTCCCGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450
GCCCACTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCACTGGAT 1500
GCCGGGCCCG ACACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550
GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600
GGGTCTTTTC AAACATAGAC AATCATGGGA TATTAAACTT GAAGGACAAT 1650
AGAGATCATC TAGTCCCATC AACTCACTAT ATATATGAGG AACCTGAGGT 1700
CCAGAGTGGG GAAGTGTCTT ACCCAAGGTC ACATGGTTTC AGAGAAATTA 1750
TGTTGAATCC AATAAGCCTT CCCGGACATT CCAAGCCTCT TAACCATGGC 1800
ATCTATGTTG AGGATGTCAA TGTTTATTTC AGCAAAGGAC GTCATGGCCT 1850
TTAAAAAC 1858

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Val Ser Leu Cys Pro Ala Lys Cys Ser Phe Trp Arg Ile
1 5 10 15

Phe Leu Leu Gly Ser Val Trp Leu Asp Tyr Val Gly Ser Val Leu
20 25 30

Ala Cys Pro Ala Asn Cys Val Cys Ser Lys Thr Glu Ile Asn Cys
35 40 45

Arg Arg Pro Asp Asp Gly Asn Leu Phe Pro Leu Leu Glu Gly Gln
 50 55 60

Asp Ser Gly Asn Ser Asn Gly Asn Ala Asn Ile Asn Ile Thr Asp
 65 70 75

Ile Ser Arg Asn Ile Thr Ser Ile His Ile Glu Asn Trp Arg Ser
 80 85 90

Leu His Thr Leu Asn Ala Val Asp Met Glu Leu Tyr Thr Gly Leu
 95 100 105

Gln Lys Leu Thr Ile Lys Asn Ser Gly Leu Arg Ser Ile Gln Pro
 110 115 120

Arg Ala Phe Ala Lys Asn Pro His Leu Arg Tyr Ile Asn Leu Ser
 125 130 135

Ser Asn Arg Leu Thr Thr Leu Ser Trp Gln Leu Phe Gln Thr Leu
 140 145 150

Ser Leu Arg Glu Leu Gln Leu Glu Gln Asn Phe Phe Asn Cys Ser
 155 160 165

Cys Asp Ile Arg Trp Met Gln Leu Trp Gln Glu Gln Gly Glu Ala
 170 175 180

Lys Leu Asn Ser Gln Asn Leu Tyr Cys Ile Asn Ala Asp Gly Ser
 185 190 195

Gln Leu Pro Leu Phe Arg Met Asn Ile Ser Gln Cys Asp Leu Pro
 200 205 210

Glu Ile Ser Val Ser His Val Asn Leu Thr Val Arg Glu Gly Asp
 215 220 225

Asn Ala Val Ile Thr Cys Asn Gly Ser Gly Ser Pro Leu Pro Asp
 230 235 240

Val Asp Trp Ile Val Thr Gly Leu Gln Ser Ile Asn Thr His Gln
 245 250 255

Thr Asn Leu Asn Trp Thr Asn Val His Ala Ile Asn Leu Thr Leu
 260 265 270

Val Asn Val Thr Ser Glu Asp Asn Gly Phe Thr Leu Thr Cys Ile
 275 280 285

Ala Glu Asn Val Val Gly Met Ser Asn Ala Ser Val Ala Leu Thr
 290 295 300

Val Tyr Tyr Pro Pro Arg Val Val Ser Leu Glu Glu Pro Glu Leu
 305 310 315

Arg Leu Glu His Cys Ile Glu Phe Val Val Arg Gly Asn Pro Pro
 320 325 330

Pro Thr Leu His Trp Leu His Asn Gly Gln Pro Leu Arg Glu Ser
 335 340 345
 Lys Ile Ile His Val Glu Tyr Tyr Gln Glu Gly Glu Ile Ser Glu
 350 355 360
 Gly Cys Leu Leu Phe Asn Lys Pro Thr His Tyr Asn Asn Gly Asn
 365 370 375
 Tyr Thr Leu Ile Ala Lys Asn Pro Leu Gly Thr Ala Asn Gln Thr
 380 385 390
 Ile Asn Gly His Phe Leu Lys Glu Pro Phe Pro Glu Ser Thr Asp
 395 400 405
 Asn Phe Ile Leu Phe Asp Glu Val Ser Pro Thr Pro Pro Ile Thr
 410 415 420
 Val Thr His Lys Pro Glu Glu Asp Thr Phe Gly Val Ser Ile Ala
 425 430 435
 Val Gly Leu Ala Ala Phe Ala Cys Val Leu Leu Val Val Leu Phe
 440 445 450
 Val Met Ile Asn Lys Tyr Gly Arg Arg Ser Lys Phe Gly Met Lys
 455 460 465
 Gly Pro Val Ala Val Ile Ser Gly Glu Glu Asp Ser Ala Ser Pro
 470 475 480
 Leu His His Ile Asn His Gly Ile Thr Thr Pro Ser Ser Leu Asp
 485 490 495
 Ala Gly Pro Asp Thr Val Val Ile Gly Met Thr Arg Ile Pro Val
 500 505 510
 Ile Glu Asn Pro Gln Tyr Phe Arg Gln Gly His Asn Cys His Lys
 515 520 525
 Pro Asp Thr Trp Val Phe Ser Asn Ile Asp Asn His Gly Ile Leu
 530 535 540
Asn Leu Lys Asp Asn Arg Asp His Leu Val Pro Ser Thr His Tyr
 545 550 555
 Ile Tyr Glu Glu Pro Glu Val Gln Ser Gly Glu Val Ser Tyr Pro
 560 565 570
 Arg Ser His Gly Phe Arg Glu Ile Met Leu Asn Pro Ile Ser Leu
 575 580 585
 Pro Gly His Ser Lys Pro Leu Asn His Gly Ile Tyr Val Glu Asp
 590 595 600
 Val Asn Val Tyr Phe Ser Lys Gly Arg His Gly Phe
 605 610 612

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 amino acids
- (B) TYPE: Amino Acid
- (C) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Leu	Arg	Gly	Gly	Arg	Arg	Gly	Gln	Leu	Gly	Trp	His	Ser	Trp
1				5					10					15
Ala	Ala	Gly	Pro	Gly	Ser	Leu	Leu	Ala	Trp	Leu	Ile	Leu	Ala	Ser
					20					25				30
Ala	Gly	Ala	Ala	Pro	Cys	Pro	Asp	Ala	Cys	Cys	Pro	His	Gly	Ser
					35				40					45
Ser	Gly	Leu	Arg	Cys	Thr	Arg	Asp	Gly	Ala	Leu	Asp	Ser	Leu	His
					50				55					60
His	Leu	Pro	Gly	Ala	Glu	Asn	Leu	Thr	Glu	Leu	Tyr	Ile	Glu	Asn
					65				70					75
Gln	Gln	His	Leu	Gln	His	Leu	Glu	Leu	Arg	Asp	Leu	Arg	Gly	Leu
					80				85					90
Gly	Glu	Leu	Arg	Asn	Leu	Thr	Ile	Val	Lys	Ser	Gly	Leu	Arg	Phe
					95				100					105
Val	Ala	Pro	Asp	Ala	Phe	His	Phe	Thr	Pro	Arg	Leu	Ser	Arg	Leu
					110				115					120
Asn	Leu	Ser	Phe	Asn	Ala	Leu	Glu	Ser	Leu	Ser	Trp	Lys	Thr	Val
					125				130					135
Gln	Gly	Leu	Ser	Leu	Gln	Glu	Leu	Val	Leu	Ser	Gly	Asn	Pro	Leu
					140				145					150
His	Cys	Ser	Cys	Ala	Leu	Arg	Trp	Leu	Gln	Arg	Trp	Glu	Glu	
					155				160					165
Gly	Leu	Gly	Gly	Val	Pro	Glu	Gln	Lys	Leu	Gln	Cys	His	Gly	Gln
					170				175					180
Gly	Pro	Leu	Ala	His	Met	Pro	Asn	Ala	Ser	Cys	Gly	Val	Pro	Thr
					185				190					195
Leu	Lys	Val	Gln	Val	Pro	Asn	Ala	Ser	Val	Asp	Val	Gly	Asp	Asp
					200				205					210
Val	Leu	Leu	Arg	Cys	Gln	Val	Glu	Gly	Arg	Gly	Leu	Glu	Gln	Ala
					215				220					225
Gly	Trp	Ile	Leu	Thr	Glu	Leu	Glu	Gln	Ser	Ala	Thr	Val	Met	Lys
					230				235					240

Ser Gly Gly Leu Pro Ser Leu Gly Leu Thr Leu Ala Asn Val Thr
 245 250 255
 Ser Asp Leu Asn Arg Lys Asn Leu Thr Cys Trp Ala Glu Asn Asp
 260 265 270
 Val Gly Arg Ala Glu Val Ser Val Gln Val Asn Val Ser Phe Pro
 275 280 285
 Ala Ser Val Gln Leu His Thr Ala Val Glu Met His His Trp Cys
 290 295 300
 Ile Pro Phe Ser Val Asp Gly Gln Pro Ala Pro Ser Leu Arg Trp
 305 310 315
 Leu Phe Asn Gly Ser Val Leu Asn Glu Thr Ser Phe Ile Phe Thr
 320 325 330
 Glu Phe Leu Glu Pro Ala Ala Asn Glu Thr Val Arg His Gly Cys
 335 340 345
 Leu Arg Leu Asn Gln Pro Thr His Val Asn Asn Gly Asn Tyr Thr
 350 355 360
 Leu Leu Ala Ala Asn Pro Phe Gly Gln Ala Ser Ala Ser Ile Met
 365 370 375
 Ala Ala Phe Met Asp Asn Pro Phe Glu Phe Asn Pro Glu Asp Pro
 380 385 390
 Ile Pro Asp Thr Asn Ser Thr Ser Gly Asp Pro Val Glu Lys Lys
 395 400 405
 Asp Glu Thr Pro Phe Gly Val Ser Val Ala Val Gly Leu Ala Val
 410 415 420
 Phe Ala Cys Leu Phe Leu Ser Thr Leu Leu Leu Val Leu Asn Lys
 425 430 435
 Cys Gly Arg Arg Asn Lys Phe Gly Ile Asn Arg Pro Ala Val Leu
 440 445 450
Ala Pro Glu Asp Gly Leu Ala Met Ser Leu His Phe Met Thr Leu
 455 460 465
 Gly Gly Ser Ser Leu Ser Pro Thr Glu Gly Lys Gly Ser Gly Leu
 470 475 480
 Gln Gly His Ile Ile Glu Asn Pro Gln Tyr Phe Ser Asp Ala Cys
 485 490 495
 Val His His Ile Lys Arg Arg Asp Ile Val Leu Lys Trp Glu Leu
 500 505 510
 Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala Glu Cys His Asn
 515 520 525

Leu	Leu	Pro	Glu	Gln	Asp	Lys	Met	Leu	Val	Ala	Val	Lys	Ala	Leu
							530		535				540	
Lys	Glu	Ala	Ser	Glu	Ser	Ala	Arg	Gln	Asp	Phe	Gln	Arg	Glu	Ala
							545		550				555	
Glu	Leu	Leu	Thr	Met	Leu	Gln	His	Gln	His	Ile	Val	Arg	Phe	Phe
				560					565				570	
Gly	Val	Cys	Thr	Glu	Gly	Arg	Pro	Leu	Leu	Met	Val	Phe	Glu	Tyr
				575				580					585	
Met	Arg	His	Gly	Asp	Leu	Asn	Arg	Phe	Leu	Arg	Ser	His	Gly	Pro
				590				595					600	
Asp	Ala	Lys	Leu	Leu	Ala	Gly	Gly	Glu	Asp	Val	Ala	Pro	Gly	Pro
				605				610					615	
Leu	Gly	Leu	Gly	Gln	Leu	Leu	Ala	Val	Ala	Ser	Gln	Val	Ala	Ala
				620				625					630	
Gly	Met	Val	Tyr	Leu	Ala	Gly	Leu	His	Phe	Val	His	Arg	Asp	Leu
				635				640					645	
Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Gln	Gly	Leu	Val	Val	Lys	Ile
				650				655					660	
Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Ile	Tyr	Ser	Thr	Asp	Tyr	Tyr
				665				670					675	
Arg	Val	Gly	Gly	Arg	Thr	Met	Leu	Pro	Ile	Arg	Trp	Met	Pro	Pro
				680				685					690	
Glu	Ser	Ile	Leu	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp	Val	Trp
				695				700					705	
Ser	Phe	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly	Lys	Gln
				710				715					720	
Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Thr	Glu	Ala	Ile	Asp	Cys	Ile	Thr
				725				730					735	
<u>Gln</u>	<u>Gly</u>	<u>Arg</u>	<u>Glu</u>	<u>Leu</u>	<u>Glu</u>	<u>Arg</u>	<u>Pro</u>	<u>Arg</u>	<u>Ala</u>	<u>Cys</u>	<u>Pro</u>	<u>Pro</u>	<u>Glu</u>	<u>Val</u>
				740				745					750	
Tyr	Ala	Ile	Met	Arg	Gly	Cys	Trp	Gln	Arg	Glu	Pro	Gln	Gln	Arg
				755				760					765	
His	Ser	Ile	Lys	Asp	Val	His	Ala	Arg	Leu	Gln	Ala	Leu	Ala	Gln
				770				775					780	
Ala	Pro	Pro	Val	Tyr	Leu	Asp	Val	Leu	Gly					
				785				790						

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGYGAYATHA TGTGGYTNAA RAC 23

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGATGCARY TNTGGCARCA RCA 23

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

YTCRTCYTTN CCRTAYTCRT T 21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCYTCYTGR RTAYTCNAC GTG 23

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CACGTCAACA ACGGCAACTA CA 22

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAGGATGA GAAACAGATT TCTGC 25

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATCAATGGC CACTTCCTCA AGG 23

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTGTTTCG TCCTTCTTCT CC 22

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGATGTGCC CGACCGGTTG TATC 24

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACAGTGATA GGAGGTGTGG GA 22

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATGTGGCT CCAGGCC 19

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGCAACCCG CCCACGGAA 19

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACGCCAGGCC AAGGGTGAG 19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAACCACTCC CAGCCCCTGG 20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTGGTGGCCT CCAGCGGCAG 20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AATTCATGAC CACCAGCCAC CA 22

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCTCCTCGGG ACTGCGATGC 20

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGTCGCCCT GGCGAGGTG GCAT 24

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTCAACA GCCAGAACCT C 21

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGCTCTGTG AGGATCCAGC C 21

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCGACCGGTT TTATCAGTGA C 21

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGATCTTGG ACTCCCGCAG AGG 23

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTTGGCCAAG GCATCTCCGG T 21

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTGCAGCA CATTAAGAGG A 21

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTATACACAG GCTTAAGCCA TCCA 24

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGAGGCATC CAGCGAATG 19

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Glu Ser Thr Asp Asn Phe Ile Leu Phe
1 5 9

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Leu Phe Asn Pro Ser Gly Asn Asp Phe Cys Ile Trp Cys Glu
1 5 10 14

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCTCCTTCTC GCCGGTGG 18

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Pro Ser Arg Arg Trp
1 5 6

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Phe Val Leu Phe His Lys Ile Pro Leu Asp Gly
1 5 10 11

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Trp	Val	Phe	Ser	Asn	Ile	Asp	Asn	His	Gly	Ile	Leu	Asn	Leu	Lys
1														15
Asp	Asn	Arg	Asp	His	Leu	Val	Pro	Ser	Thr	His	Tyr	Ile	Tyr	Glutamic acid
														30
Glu	Pro	Glu	Val	Gln	Ser	Gly	Glu	Val	Ser	Tyr	Pro	Arg	Ser	His
														45
Gly	Phe	Arg	Glu	Ile	Met	Leu	Asn	Pro	Ile	Ser	Leu	Pro	Gly	His
														60
Ser	Lys	Pro	Leu	Asn	His	Gly	Ile	Tyr	Val	Glu	Asp	Val	Asn	Val
														75
Tyr	Phe	Ser	Lys	Gly	Arg	His	Gly	Phe						
									80	84				

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